



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:

Perryman, Benjamin M., *et al.*

Serial No.: 10/697,991

Filed: 10/30/2003

For: QUANTITATIVE ANALYSIS OF
PROTEIN ISOFORMS USING MATRIX-
ASSISTED LASER
DESORPTION/IONIZATION TIME OF
FLIGHT MASS SPECTROMETRY

Group Art Unit: 1743

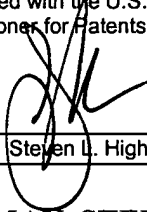
Examiner Gakh, Yelena G.

Atty. Dkt. No.: MYOG:056US

CERTIFICATE OF MAILING
37 C.F.R. § 1.8

I hereby certify that this correspondence is being deposited with the U.S. Postal Service with sufficient postage as First Class Mail in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, Va 22313-01450, on the date below:

January 19, 2005
Date


Steven L. Highlander

DECLARATION OF M. BENJAMIN PERRYMAN, STEVE M. HELMKE AND MARK W.

DUNCAN UNDER 37 C.F.R. §1.131

Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-01450

Dear Sir:

We, M. Benjamin Perryman, Steve M. Helmke, and Mark W. Duncan, do declare the following:

1. M. Benjamin Perryman is a citizen of the United States. M. Benjamin Perryman resides at 25638 487th Avenue, Garretson, SD 57030, and currently holds the position of Director at South Dakota Health Research Foundation, Sioux Falls, SD. Steve M. Helmke is a citizen of the United States. Steve Helmke resides at 2737 Hooker Street, Denver, CO 80211, and currently holds the position of Instructor at the University of

Colorado, Denver, CO. Mark W. Duncan is a citizen of Australia. Mark W. Duncan resides at 4550 Lowell Blvd., Denver, CO 80211, and currently holds the position of Professor at the University of Colorado.

2. We are the named inventors in the above-captioned application, U.S. Serial No. 10/697,991, entitled "QUANTITATIVE ANALYSIS OF PROTEIN ISOFORMS USING MATRIX-ASSISTED LASER DESORPTION/IONIZATION TIME OF FLIGHT MASS SPECTROMETRY."
3. We began work using MALDI-TOF for protein isoform analysis prior to Jan. 15, 2002, as evidenced by the papers attached.
4. I hereby declare that all statements made of my own knowledge are true and all statements made on information are believed to be true and further that the statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment or both under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of this application or any patent issued thereon.

Jan. 18, 2005

Date

M. Benjamin Perryman

M. Benjamin Perryman

Date

Steve M. Helmke

Colorado, Denver, CO. Mark W. Duncan is a citizen of Australia. Mark W. Duncan resides at 4550 Lowell Blvd., Denver, CO 80211, and currently holds the position of Professor at the University of Colorado.

2. We are the named inventors in the above-captioned application, U.S. Serial No. 10/697,991, entitled "QUANTITATIVE ANALYSIS OF PROTEIN ISOFORMS USING MATRIX-ASSISTED LASER DESORPTION/IONIZATION TIME OF FLIGHT MASS SPECTROMETRY."
3. We began work using MALDI-TOF for protein isoform analysis prior to Jan. 15, 2002, as evidenced by the papers attached.
4. I hereby declare that all statements made of my own knowledge are true and all statements made on information are believed to be true and further that the statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment or both under § 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of this application or any patent issued thereon.

Date

1-18-05

Date

M. Benjamin Perryman

Steve M. Helmke

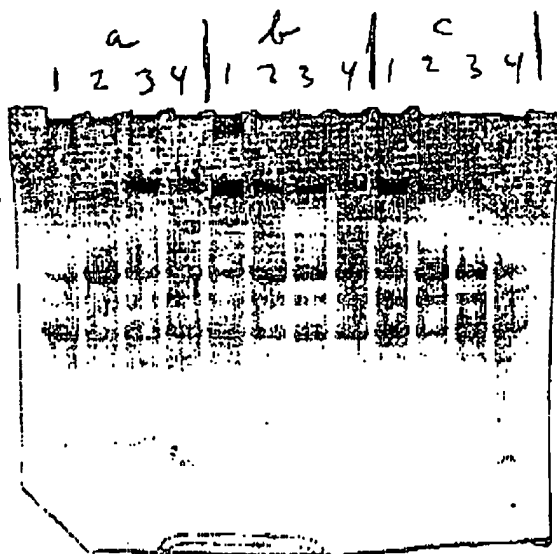
Steve M. Helmke

1/18/51
Date

Mark W. Duncan
Mark W. Duncan

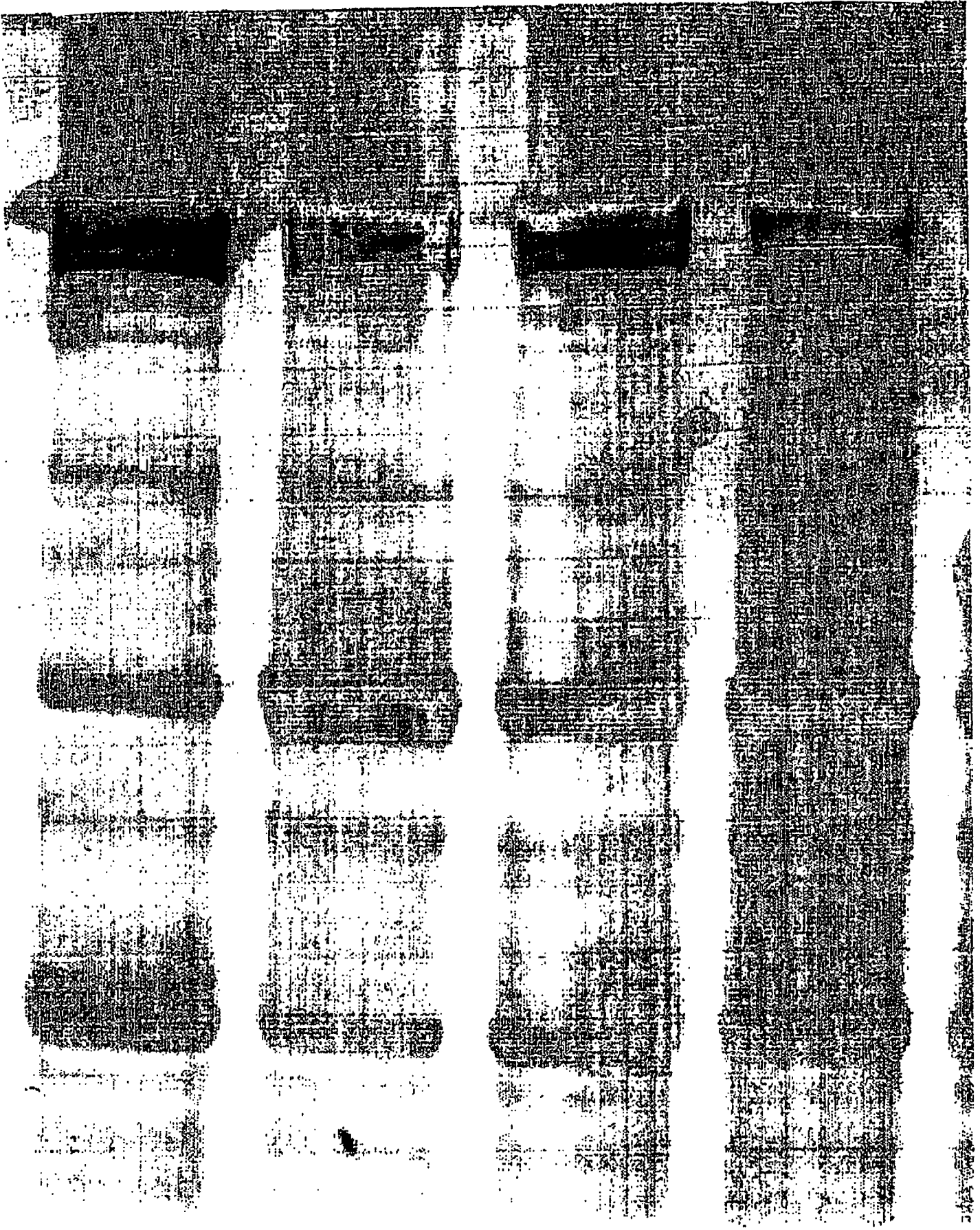


myosin



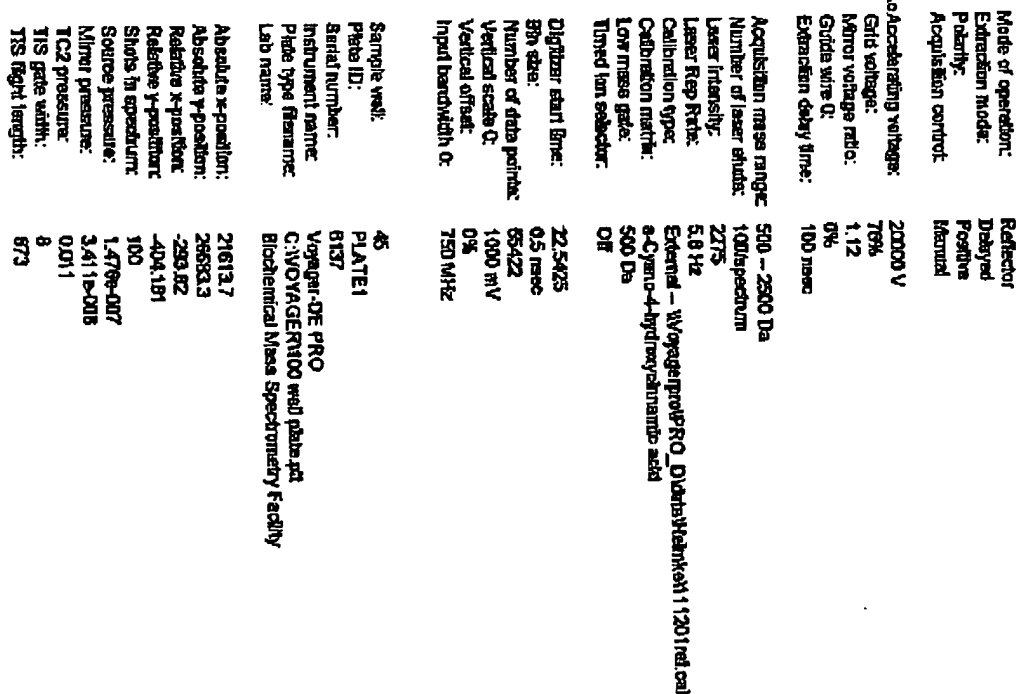
		<u>% α-MyHC (By Az stain)</u>
1	SMC 18	13
2	Spencer	25
3	GJ1	56
4	Arner	71

BEST AVAILABLE COPY



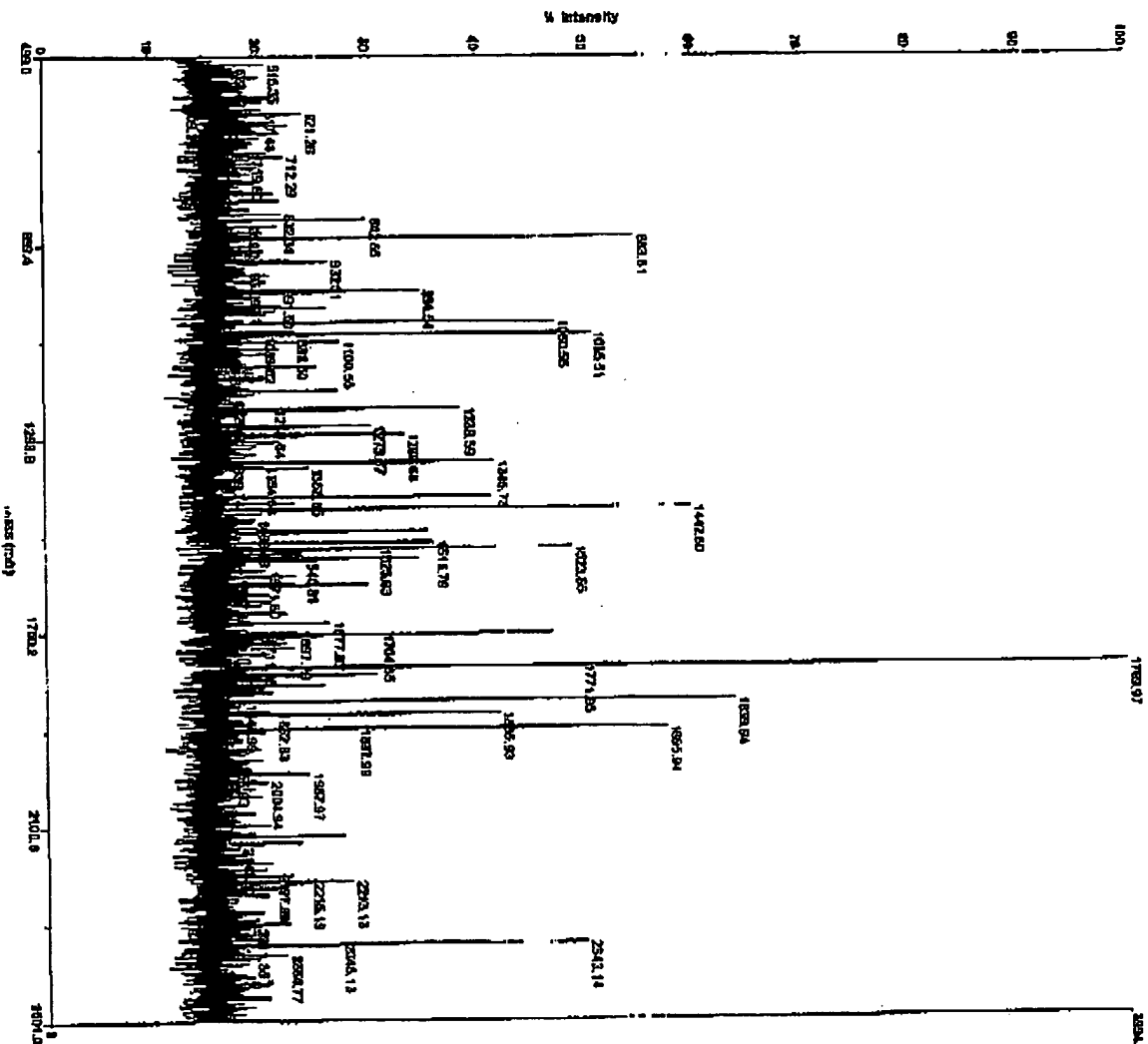
BEST AVAILABLE COPY

Voyager Spec #1 [BP = 17409, 2155]



Applied Biosystems Voyager System 6137

Voyager Spec #1111P = 1770.0, 3860



Mode of operation:	Reflector
Extraction mode:	Delayed
Polarity:	Positive
Acquisition control:	Manual
Grid voltage:	20000 V
Mirror voltage ratio:	75%
Guide wire D:	1.12
Extraction delay time:	0%
Acquisition mass range:	500 - 2500 Da
Number of laser shots:	100/spectrum
Laser intensity:	2275
Laser Rep Rate:	5.6 Hz
Calibration type:	External - W/peptide/PRO, Dithiothreitol 111201mol/mol
Calibration method:	p-Cyano-4-hydroxycinnamic acid
Low mass gate:	500 Da
Timed ion selector:	Off
Digital start time:	22.5425
Bin size:	0.5 msec
Number of data points:	55422
Vertical scale D:	1000 mV
Vertical offset:	0%
Input bandwidth D:	750 MHz
Sample well:	44
Plate ID:	PLATE1
Serial number:	6137
Instrument name:	Voyager-DE PRO
Plate type filename:	C:\VOYAGER\101 well plate.pr
Lab name:	Biochemical Mass Spectrometry Facility
Absolute x-position:	16828.7
Absolute y-position:	28887.5
Relative x-position:	1.18684
Relative y-position:	0.00833849
Shots in spectrum:	100
Source pressure:	1.44E-007
Mirror pressure:	3.428E-008
TIS gate width:	0.01105
TIS flight length:	8
	873

BEST AVAILABLE COPY

Applied Biosystems Voyager System 6137

Voyager Spec #10>LCTBP = 1798.9, 8341)

Mode of operation:	Reflect
Excitation mode:	Delayed
Polarity:	Positive
Acquisition control:	Manual

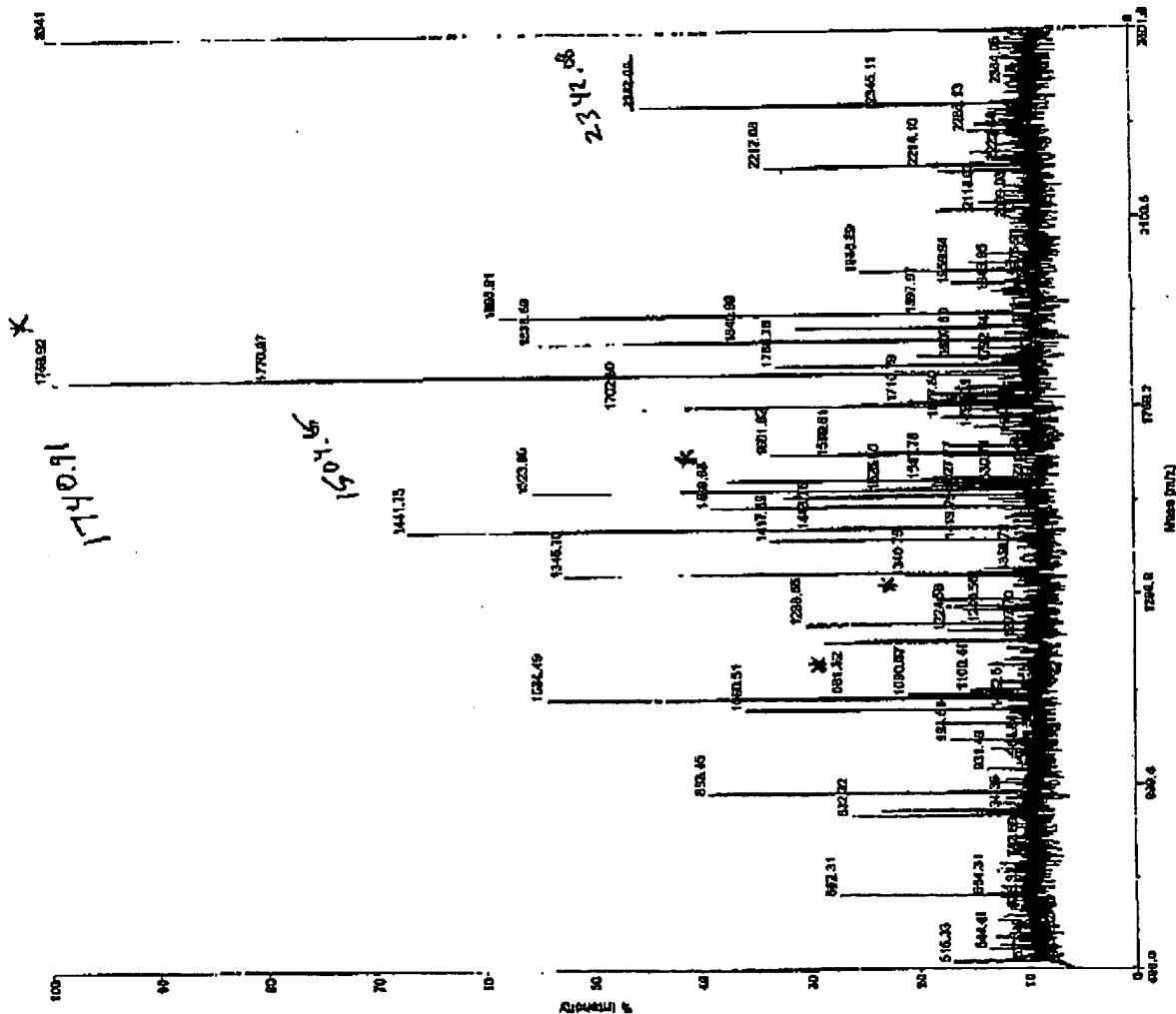
Accelerating voltage:	200kV V
Grid voltage:	76%
Mirror voltage ratio:	1.12
Guide wire α	0%
Extraction delay time:	160 nsec

Acquisition mass range:	500 – 2500 Da
Number of laser shots:	100/spectrum
Laser intensity:	2144
Laser Rep Rate:	5.8 Hz
Calibration type:	External – W/O
Calibration matrix:	α -Cyano-4-hydroxybenzoic acid
Low mass gate:	500 Da
Timed ion selector:	Off

Digitizer start time:	22.542
Eligible size:	0.5 nsec
Number of data points:	55420
Vertical scale 0:	1000 mV
Vertical offset:	0%
Low bandwidth 0:	750 kHz

Sample well:
Plate ID:
Serial number:
Instrument name:
Plate type filename:
Lab name:

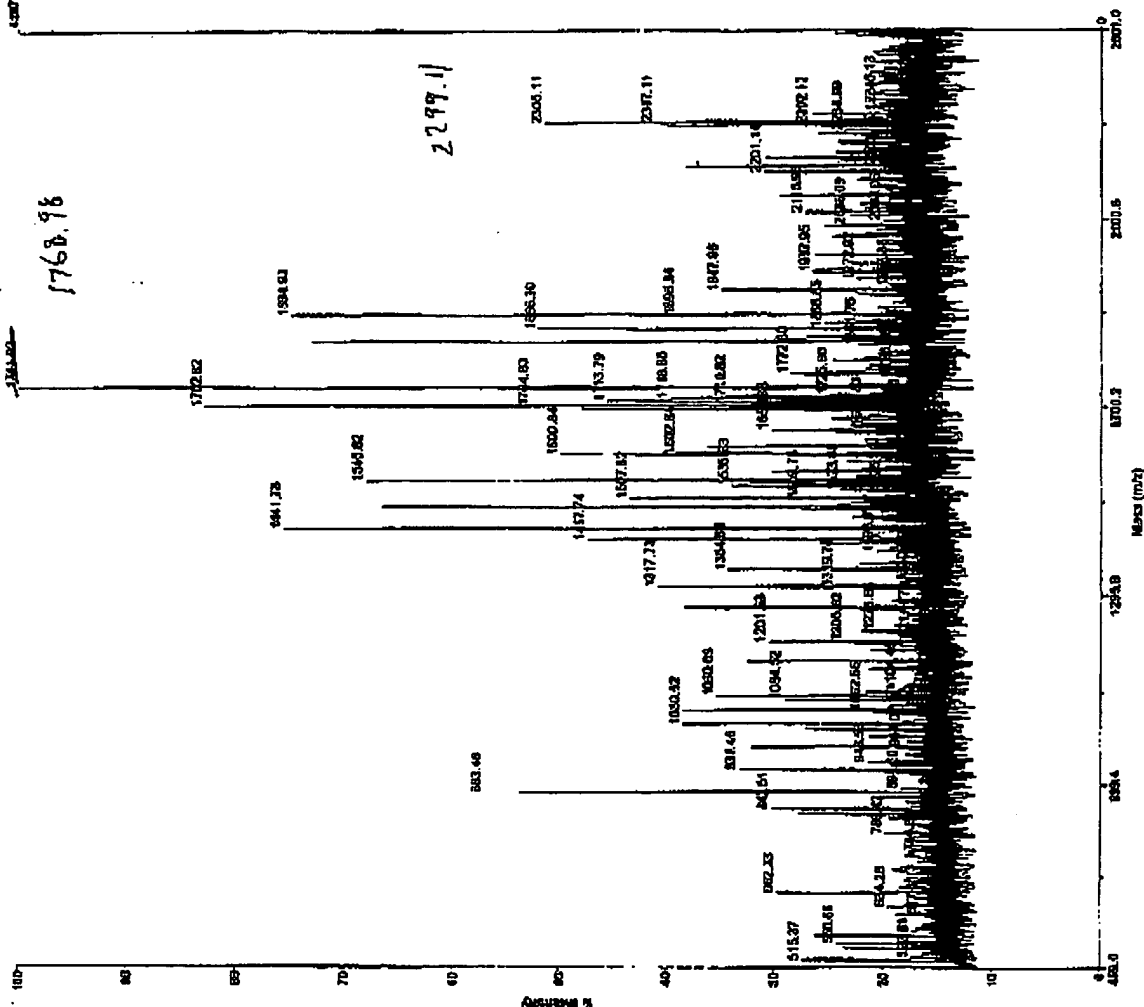
Absolute x-position:	17473.5
Absolute y-position:	16881.3
Relative x-position:	648.011
Relative y-position:	-148.155
Slits in spectrum:	100
Source pressure:	1.789e-01
Mirror pressure:	4.514e-01
TG2 pressure:	0.01182
TIS gate width:	8
TIS slit length:	573



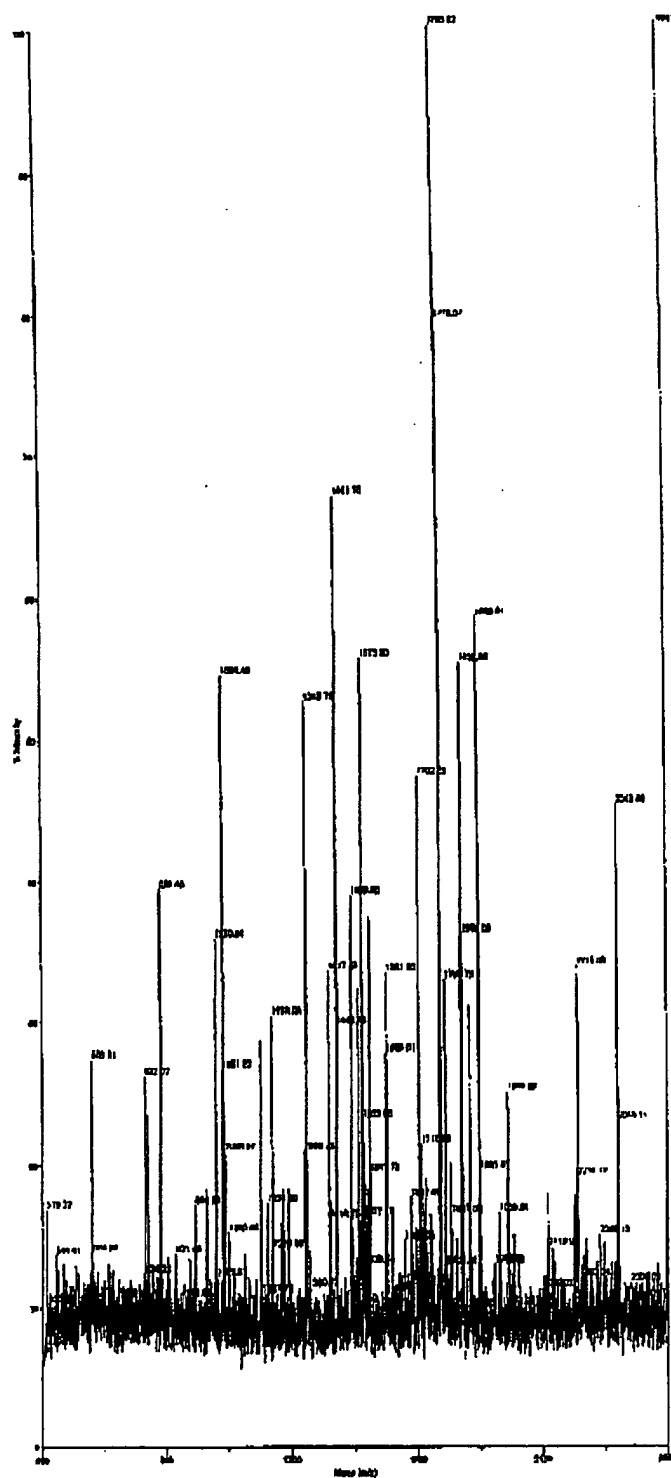
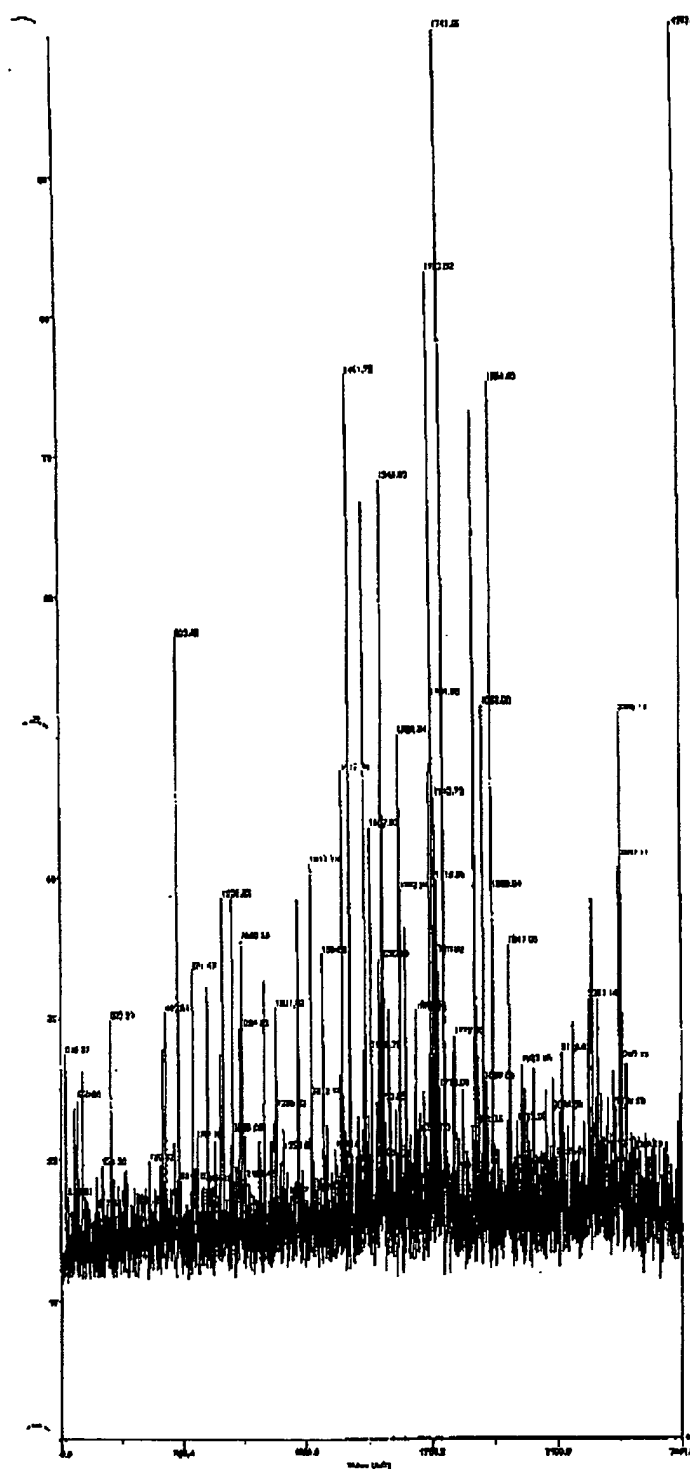
BEST AVAILABLE COPY

Applied Biosystems Voyager System 6137

Voyager Spec #100 MC [BP] = 1241.8, 42880



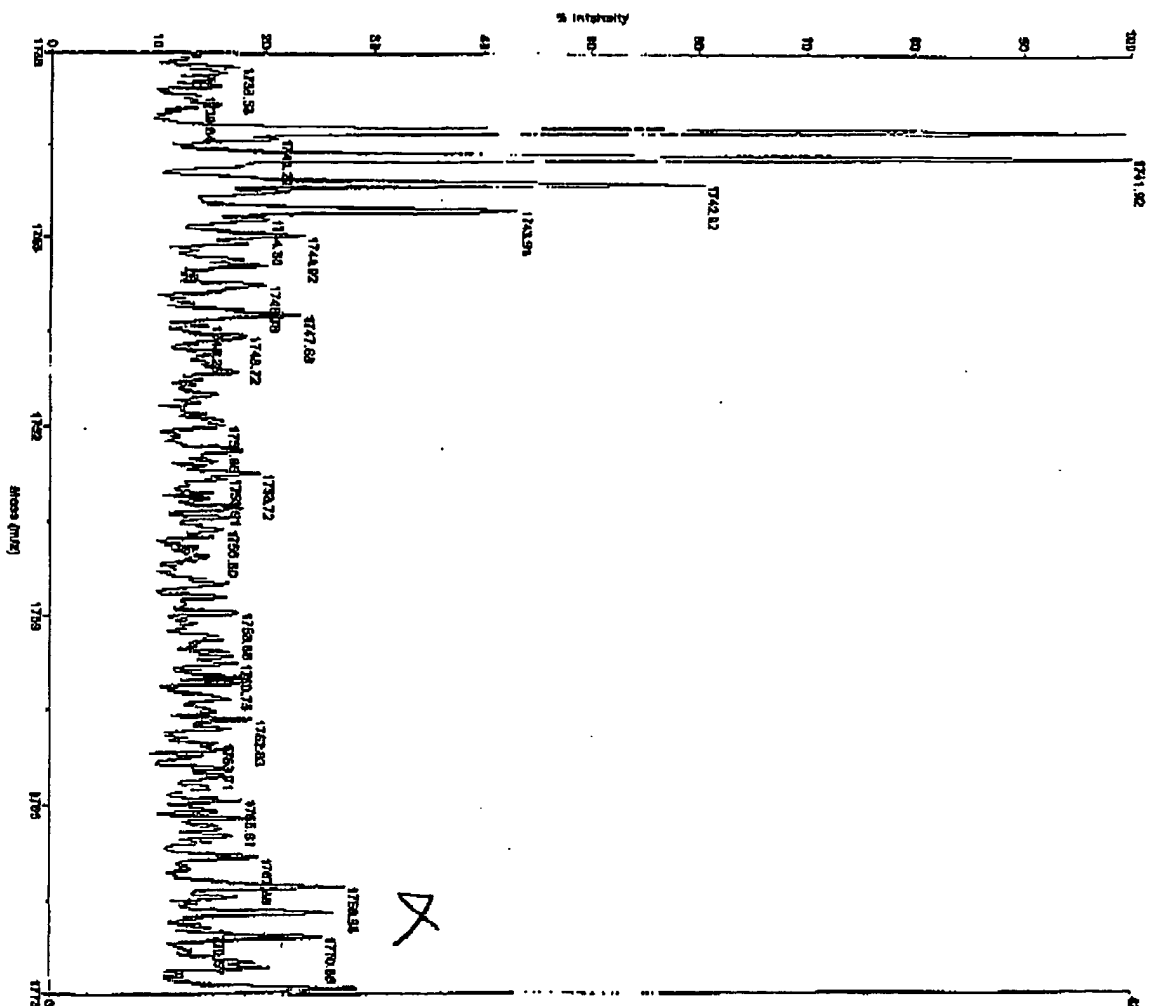
Wagner Type S1 MOPF = 172.8, 634.7



BEST AVAILABLE COPY

13
1740.94

13
1740.94



Reflector Dryed Positive Manual

20000 Y
7500

1.12

100 ms

500 - 2500 Da

1949

External - \\vovagisrpt\PRO_Data\Hb\HbKey\11301_0001.cali

500 Da

44

0.5 TREAT

1050 ml

750 MHz

PLATE 1

Voyager-

Biochemical Mass Spectrometry Facility

21540

2100.1
367.471

100

3.816e-0

Q
3

673

2

2

4

1

20

SP. sample high in β -myth protein
has high β protein and
low α protein amount
 \therefore quantitate by MAB1

